



Appl. No. 09/905,666
Amdt. Dated April 1, 2004
Reply to Office Action of October 1, 2003
Annotated Sheet Showing Changes

SEQ: 001-405 (pumillas)	(1)	-----ATGAAATTGTAAAAAGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCAAGTCACATCGC
SEQ: 002-406 (subtilis)	(1)	-----ATGAAATTGTAAAAAGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC
SEQ: 003-402 (megat.)	(1)	-----ATGAAATTGTAAAAAGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCAAGTCACATCGC
SEQ: 004-400 (ventus)	(1)	-----ATGAAATTGTAAAAAGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCAAGTCACATCGC
SEQ: 005-396 (circul.)	(1)	-----ATGAAATTGTAAAAAGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCAAGTCACATCGC
SEQ: 006-392 (azotof.)	(1)	-----ATGAAATTGTAAAAAGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCAAGTCACATCGC
SEQ: 007-398 (firmus)	(1)	-----ATGAAATTGTAAAAAGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCAAGTCACATCGC
SEQ: 008-393 (badius)	(1)	-----ATGAAATTGTAAAAAGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCAAGTCACATCGC
SEQ: 009-405a	(1)	-----ATGAAATTGTAAAAAGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC
SEQ: 010-405f	(1)	-----ATGAAATTGTAAAAAGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC
SEQ: 011-405g	(1)	ATGAAAGTGATTTTGTAAAGAAAAAGGAGT-TTGCAAAATCTTGTTGCCCTTGCCCTTAGTGCTAGGTTCAATAGC
SEQ: 012-405A2	(1)	ATGAAAGTGATTTTGTAAAGAAAAAGGAGT-TTGCAAAATCTTGTTGCCCTTGCCCTTAGTGCTAGGTTCAATAGC
SEQ: 013-405I2	(1)	ATGAAAGTGATTTTGTAAAGAAAAAGGAGT-TTGCAAAATCTTGTTGCCCTTGCCCTTAGTGCTAGGTTCAATAGC
SEQ: 014-405a	(1)	-----ATGAAATTGTAAAAAGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC
SEQ: 015-405c	(1)	-----ATGAAATTGTAAAAAGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC
SEQ: 016-405d	(1)	-----ATGAAATTGTAAAAAGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC
SEQ: 017-405f	(1)	-----ATGAAATTGTAAAAAGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC
SEQ: 018-405h	(1)	-----ATGAAATTGTAAAAAGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC
SEQ: 019-405b1	(1)	ATGAAAGTGATTTTGTAAAGAAAAAGGAGT-TTGCAAAATCTTGTTGCCCTTGCCCTTAGTGCTAGGTTCAATAGC
SEQ: 020-405a	(1)	-----ATGAAATTGTAAAAAGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC

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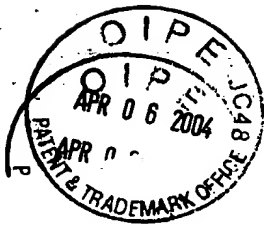
Figure 3a



2004

	(Signal peptide coding region)	(Mature coding region)
SEQ: 001-405 (pumilus)	76	150
SEQ: 002-406 (subtilis)	(65) TGTTCGCGTTCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTGTGTTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 003-402 (megat.)	(65) TGTTCGCGTTCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTGTGTTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 004-400 (lentus)	(65) TGTTCGCGTTCAGCCGTCAGCAAAAGCCGCT	GA - CACAATCCAGTGTGTTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 005-396 (circul.)	(65) TGTTCGCGTTCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTGTGTTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 006-392 (axotof.)	(65) TGTTCGCGTTCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTGTGTTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 007-398 (firmus)	(65) TGTTCGCGTTCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTGTGTTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 008-393 (badius)	(65) TGTTCGCGTTCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTGTGTTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 009-Dc5h	(65) TGTTCGCGTTCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTGTGTTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 010-Dc5f	(65) TGTTCGCGTTCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTGTGTTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 011-Dc5c1	(75) CTTTCATCCAGCCGAAAGAGATCAGA - GCGGCT	GAGCATAATCCGCTTGTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 012-Dc5a2	(75) CTTTCATCCAGCCGAAAGAGATCAGA - GCGGCT	GAGCATAATCCGCTTGTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 013-Dc512	(75) GTTTATCCAGCCGAAAGAGGCGAAG - GCGGCT	GAGCATAATCCGCTTGTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 014-Sga	(65) TGTTCGCGTTCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTGTGTTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 015-Sgc	(65) TGTTCGCGTTCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTGTGTTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 016-Sgd	(65) TGTTCGCGTTCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTGTGTTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 017-Sgf	(65) TGTTCGCGTTCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTGTGTTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 018-Sgh	(65) TGTTCGCGTTCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTGTGTTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 019-Mt2b1	(75) CTTTCATCCAGCCGAAAGAGATCAGA - GCGGCT	GAGCATAATCCGCTTGTATGGTTTCAC - GGTATCGGAGGAGCT
SEQ: 020-H2a	(65) TGTTCGCGTTCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTGTGTTATGGTTTCAC - GGTATCGGAGGAGCT

Figure 3b



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delete

151
SEQ: 001-405 (pumilus) (139) TCATACAAATTTTGGGGAATTAAAGAGCTATCTCGTATCTCAGGGCTGGTACGGGGCAAGCTGTATGCGGTTGAT
SEQ: 002-406 (subtilis) (139) TCATTCAATTTTGGGGAATTAAAGAGCTATCTCGTATCTCAGGGCTGGTACGGGGCAAGCTGTATGCGGTTGAT
SEQ: 003-402 (megat) (139) TCATACAAATTTTGGGGAATTAAAGAGCTATCTCGTATCTCAGGGCTGGTACGGGGCAAGCTGTATGCGGTTGAT
SEQ: 004-400 (latus) (139) TCATACAAATTTTGGGGAATTAAAGAGCTATCTCGTATCTCAGGGCTGGTACGGGGCAAGCTGTATGCGGTTGAT
SEQ: 005-396 (circul) (139) TCATACAAATTTTGGGGAATTAAAGAGCTATCTCGTATCTCAGGGCTGGTACGGGGCAAGCTGTATGCGGTTGAT
SEQ: 006-392 (azotof) (139) TCATACAAATTTTGGGGAATTAAAGAGCTATCTCGTATCTCAGGGCTGGTACGGGGCAAGCTGTATGCGGTTGAT
SEQ: 007-398 (firmus) (139) TCATACAAATTTTGGGGAATTAAAGAGCTATCTCGTATCTCAGGGCTGGTACGGGGCAAGCTGTATGCGGTTGAT
SEQ: 008-393 (badius) (139) TCATACAAATTTTGGGGAATTAAAGAGCTATCTCGTATCTCAGGGCTGGTACGGGGCAAGCTGTATGCGGTTGAT
SEQ: 009-Dc5h
SEQ: 010-Dc5f
SEQ: 011-Dc5c1
SEQ: 012-Dc5a2
SEQ: 013-Dc5l2
SEQ: 014-Sga
SEQ: 015-Sgc
SEQ: 016-Sgd
SEQ: 017-Sgf
SEQ: 018-Sgh
SEQ: 019-Mt2b1
SEQ: 020-H2a
225

Figure 3c

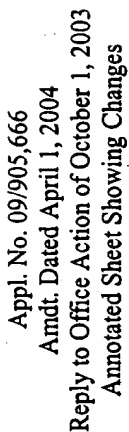


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226
SEQ: 001-405 (pumilus) (214) TTTTGGGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATACAGATTTGTGCAAAAGGTTTGTAGACGAA
SEQ: 002-406 (subtilis) (214) TTTTGGGACAAAGACAGGGACGAATTATAACAATGGACCGGTATTACACGATTTGTGCAAAAGGTTTGTAGATGAA
SEQ: 003-407 (megat.) (214) TTTTGGGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACGAA
SEQ: 004-408 (lentus) (214) TTTTGGGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACGAA
SEQ: 005-396 (cixcul.) (214) TTTTGGGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACGAA
SEQ: 006-392 (azobof.) (214) TTTTGGGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACGAA
SEQ: 007-398 (firmus) (214) TTTTGGGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACGAA
SEQ: 008-393 (badius) (214) TTTTGGGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGATGAA
SEQ: 009-105 (214) TTCAAGGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACAAA
SEQ: 010-105 (214) TTCTAAGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACAAA
SEQ: 011-105 (223) TTCTAAGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACAAA
SEQ: 012-105 (223) TTCTAAGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACAAA
SEQ: 013-105 (223) TTCTAAGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACAAA
SEQ: 014-105 (214) TTCTAAGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACAAA
SEQ: 015-105 (214) TTCTAAGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACAAA
SEQ: 016-105 (214) TTCTAAGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACAAA
SEQ: 017-105 (214) TTCTAAGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACAAA
SEQ: 018-105 (214) TTCTAAGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACAAA
SEQ: 019-105 (223) TTCTAAGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACAAA
SEQ: 020-105 (214) TTCTAAGACAAAGACAGGGACGAATTATAACAATGGCCCGGTATTATCAGATTTGTGCAAAAGGTTTGTAGACAAA

Figure 3d



301

SEQ: 001-405 (pumilus)	(289)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGTATGGGTGGCGCGAAACACACACCTTTACTACATAAAAAAATCTG
SEQ: 002-406 (subtilis)	(289)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGGGGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 003-407 (megat.)	(289)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 004-408 (lentus)	(289)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 005-409 (circul.)	(289)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 006-410 (azotof.)	(289)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 007-411 (firmus)	(289)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 008-412 (badius)	(289)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 009-413 (Dc5h)	(289)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 010-414 (Dc5f)	(289)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 011-415 (Dc5c1)	(298)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 012-416 (Dc5a2)	(298)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 013-417 (Dc512)	(298)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 014-418 (Sga)	(289)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 015-419 (Sgc)	(289)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 016-420 (Svd)	(289)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 017-421 (Sgf)	(289)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 018-422 (Sgn)	(289)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 019-423 (Mt2b1)	(298)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG
SEQ: 020-424 (H2a)	(289)	ACGGGTGCGAAAAAAGTGATATTGTCTCACAGCATGGGTGGCGCGCGAAACACACCTTTACTACATAAAAAAATCTG

Figure 3e



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20/20

SEQ:0011-406 (pumilus)	(364)	GACGGCGGAAATAAAATTGAAACGTCGTAACGCTTGGCGGGCGGAACCGTTCGACGACAAAGCGCTTCCG	376	450
SEQ:002-406 (subtilis)	(364)	GACGGCGGAAATAAAAGTTGCAACGTCGTGACGCTTGGCGGGCGGAACCGTTTGACGACAGGCAAGCGCTTCCG		
SEQ:003-402 (megat.)	(364)	GACGGCGGAAATAAAATTGAAACGTCGTAACGCTTGGCGGGCGGAACCGTTTGACGACAAAGCGCTTCCG		
SEQ:004-400 (lentus)	(364)	GACGGCGGAAATAAAATTGAAACGTCGTAACGCTTGGCGGGCGGAACCGTTTGACGACAAAGCGCTTCCG		
SEQ:005-396 (circul.)	(364)	GACGGCGGAAATAAAATTGAAACGTCGTAACGCTTGGCGGGCGGAACCGTTTGACGACAAAGCGCTTCCG		
SEQ:006-392 (azotof.)	(364)	GACGGCGGAAATAAAATTGAAACGTCGTAACGCTTGGCGGGCGGAACCGTTTGACGACAAAGCGCTTCCG		
SEQ:007-398 (firmus)	(364)	GACGGCGGAAATAAAATTGAAACGTCGTAACGCTTGGCGGGCGGAACCGTTTGACGACAAAGCGCTTCCG		
SEQ:008-393 (badius)	(364)	GACGGCGGAAATAAAATTGAAACGTCGTAACGCTTGGCGGGCGGAACCGTTTGACGACAAAGCGCTTCCG		
SEQ:009-Dc5h	(364)	GACGGCGGAAATAAAAGTTGAAACGTCGTAACGCTTGGCGGGCGGAACCGTTTGACGACAAAGCGCTTCCG		
SEQ:010-Dc5f	(364)	GATGGCGGCGATATAAAATTGAAACGTTGTACAAATTTGGTGAGCAAAACGGACTCGTTTCAAGCAGCATTAACA		
SEQ:011-Dc5c1	(373)	GACGGTGAGATATAAAATTGAAACGTCGTCACATTTAGGTGGAGCAAAACGGACTCGTATCACTCAGAGCATTAACA		
SEQ:012-Dc5a2	(373)	GACGGCGGCGATATAAAATTGAAACGTTGTGTACATTTGGTGAGCGCAACGGACTCGTTTCACTCAGAGCATTAACA		
SEQ:013-Dc512	(373)	GATGGCGGCGATATAAAATTGAAACGTTGTGTACAAATTTGGTGAGCAAAACGGACTCGTTTCAAGCAGAGCATTAACA		
SEQ:014-Sga	(364)	GATGGCGGTAATAAAATTGAAACGTCGTAACACATTTGGCGGGCGGAATCGTCTTGTGACAGGCAAGGCGCTTCCG		
SEQ:015-Sgc	(364)	GATGGCGGTAATAAAATTGAAACGTCGTAACACATTTGGCGGGCGGAATCGTCTTGTGACAGGCAAGGCGCTTCCG		
SEQ:016-Sgd	(364)	GATGGCGGTAATAAAATTGAAACGTCGTAACACATTTGGCGGGCGGAATCGTCTTGTGACAGGCAAGGCGCTTCCG		
SEQ:017-Sgf	(364)	GATGGTGCGGATATAAAATTGAAACGTTGTTCACAAATTTGGTGAGCAAAACGGACTCGTTTCAAGCAGAGCATTAACA		
SEQ:018-Sgn	(364)	GATGGTGCGGATATAAAATTGAAACGTTGTTCACAAATTTGGTGAGCAAAACGGACTCGTTTCAAGCAGAGCATTAACA		
SEQ:019-Mt2b1	(373)	GATGGCGGCGATATAAAATTGAAACGTCGTCACCAATTTGGTGAGCAAAACGGACTCGTTTCACTCAGAGCATTAACA		
SEQ:020-H2a	(364)	GATGGCGGCGATATAAAATTGAGAACGTTGTTCACAAATTTGGCGGGAGCAAAACGGACTCGTTTCAAGCAGAGCATTAACA		

Figure 3f

525

451

SEQ:001-405 (pumilus) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACAC-GCAGTGCCCGATATGATTGTCATGAATTACTT
SEQ:002-406 (subtilis) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACAC-GCAGTGCCCGATATGATTGTCATGAATTACTT
SEQ:003-402 (negat.) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACAC-GCAGTGCCCGATATGATTGTCATGAATTACTT
SEQ:004-400 (lentus) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACAC-GCAGTGCCCGATATGATTGTCATGAATTACTT
SEQ:005-396 (circul.) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACAC-GCAGTGCCCGATATGATTGTCATGAATTACTT
SEQ:006-392 (azotof.) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACAC-GCAGTGCCCGATATGATTGTCATGAATTACTT
SEQ:007-398 (firmus) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACAC-GCAGTGCCCGATATGATTGTCATGAATTACTT
SEQ:008-393 (badius) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACAC-GCAGTGCCCGATATGATTGTCATGAATTACTT
SEQ:009-Dc5h (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCGTCCTATA-GCTCAGCAGATCTTATTGTCGTCACACAGCCT
SEQ:010-Dc5f (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCGTCCTATA-GCTCAGCAGATCTTATTGTCGTCACACAGCCT
SEQ:011-Dc5c1 (448) GGCACCGATCCAAATCAAAAAGATTTTATACACATCCGTCCTATA-GCTCAGCAGATCTTATTGTCGTCACACAGCCT
SEQ:012-Dc5a2 (448) GGCACCGATCCAAATCAAAAAGATTTTATACACATCCGTCCTATA-GCTCAGCAGATCTTATTGTCGTCACACAGCCT
SEQ:013-Dc512 (448) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCGTCCTATA-GCTCAGCAGATCTTATTGTCGTCACACAGCCT
SEQ:014-Sga (439) GGTACTGATCCCAACCAAAAAGATTTGTAACACATCCGTCCTATA-GTAGTGCTGATATGATTGTTATGAATTACTT
SEQ:015-Sgc (439) GGTACTGATCCCAACCAAAAAGATTTGTAACACATCCGTCCTATA-GTAGTGCTGATATGATTGTTATGAATTACTT
SEQ:016-Sgd (439) GGTACTGATCCCAACCAAAAAGATTTGTAACACATCCGTCCTATA-GTAGTGCTGATATGATTGTTATGAATTACTT
SEQ:017-Sgf (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCGTCCTATA-GCTCAGCAGATCTTATTGTCGTCACACAGTCT
SEQ:018-Sgh (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCGTCCTATA-GCTCAGCAGATCTTATTGTCGTCACACAGTCT
SEQ:019-Mt2b1 (448) GGAACAGATCCAAATCAAAAAGATTTCTCTATACATCTGTCCTATA-GCTCAGCCGATTTGATTGTCGTCACACAGCCT
SEQ:020-H2a (439) GGCACAGATCCAAATCAAAAAGATTTCTTTTACACATCCGTCCTACAAGCTCAGCCGATCTCATTTGTCGTCACACAGTCT

Figure 39



Appl. No. 09/905,666
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526 600

SEQ:001-405 (pumilus)	(513) ATCAAAATTAGACGGT-GCTAAAAAC-GCTCAAAATTCATGGCGTTGGGCACACATTGGTTTATTGATGAACAGCCAA
SEQ:002-406 (subtilis)	(513) ATCAAGATTAGATGGT-GCTAGAAAC-GTTCAAAATCCATGGCGTTGGACACACATCGGCCCTTCTGTACAGCAGCCAA
SEQ:003-407 (megat.)	(513) ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACACATTGGTTTATTGATGAACAGCCAA
SEQ:004-400 (lentos)	(513) ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACACATTGGTTTATTGATGAACAGCCAA
SEQ:005-396 (cilicul.)	(513) ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACACATTGGTTTATTGATGAACAGCCAA
SEQ:006-392 (azotof.)	(513) ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACACATTGGTTTATTGATGAACAGCCAA
SEQ:007-398 (firmus)	(513) ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACACATTGGTTTATTGATGAACAGCCAA
SEQ:008-393 (badius)	(513) ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACACATTGGTTTATTGATGAACAGCCAA
SEQ:009-Dc5A	(513) ATCAAGATTAGATGGT-GCGAGAAAC-GTTCAAAATCCATGGCGTTGGACACATCGGCCCTTCTGTACAGCAGCCAA
SEQ:010-Dc5f	(513) CTCTCGTTTAAATTGGC-GCAAGAAAC-ATCCTGATCCATGGCGTTGGTCATATCGGTCTATTAACTCAAGCCAA
SEQ:011-Dc5c1	(522) TTCGC-GTTTAAATTGGCGCAAGAAAC-GTCTGATCCACGGCGTTGGACATATCGGTCTATTAACTCAAGCCAA
SEQ:012-Dc5a2	(522) CTCGC-GTTTAAATTGGCGCAAGAAAC-GTCTGATCCACGGCGTTGGTCACATCGGTCTATTAGCTCAAGCCAA
SEQ:013-Dc512	(522) CTCTCAGTTTAAATTGGCGCAAGAAAC-ATCCTGATCCA-GGCGTTGGTCATATCGGTCTATTAACTCAAGCCAA
SEQ:014-Sga	(513) AACAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTCGGACATATCGGCCCTTCTGTACAGCAGCCAA
SEQ:015-Sgc	(513) ATCAAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTCGGACATATCGGCCCTTCTGTACAGCAGCCAA
SEQ:016-Sga	(513) ATCAAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTCGGACATATCGGCCCTTCTGTACAGCAGCCAA
SEQ:017-Sgf	(513) CTCTCGTTTAAATTGGC-GCAAGAAAC-GTCCAAATCCATGGCGTTGGACATATCGGTCTATTAACTCAAGCCAA
SEQ:018-Sgh	(513) CTCTCGTTTAAATTGGC-GCAAGAAAC-GTCCAAATCCATGGCGTTGGACATATCGGTCTATTAACTCAAGCCAA
SEQ:019-Mt2b1	(522) TTCGC-GTTTAACTGGCGCAAGAAAT-GTCTGATCCACGGCGTTGGCCATATCGGTCTATTAACTCAAGCCAA
SEQ:020-H2a	(514) CTCTCGTTTAAATTGGCTGCAAGAAACAGTCCAAATCCATGGCGTTGGACATATCGGTCTATTAACTCAAGCCAA

Figure 3h



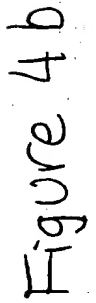
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Annotated Sheet Showing Changes

SEQ: 001-405 (pumilus)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCCAAAATACGAATTAA	601	654
SEQ: 002-406 (subtilis)	(586)	GTCAACAGCCTGATTAAAGAGGCTGAACGGCGGGGGGACTCAATACAAATTAG		
SEQ: 003-402 (megat.)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCCACAATACAAATTAA		
SEQ: 004-400 (tentus)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGACTAAATACAAATTAA		
SEQ: 005-396 (ciacul.)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGCTCAATACAAATTAA		
SEQ: 006-392 (azobof.)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGCTAGATACAAATTAA		
SEQ: 007-398 (firmus)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGCTCAATACAAATTAA		
SEQ: 008-393 (badius)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGCTCAATACAAATTAA		
SEQ: 009-391 (badius)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGCTCAATACAAATTAA		
SEQ: 010-391 (badius)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGCTCAATACAAATTAA		
SEQ: 011-391 (badius)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGCTCAATACAAATTAA		
SEQ: 012-391 (badius)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGCTCAATACAAATTAA		
SEQ: 013-391 (badius)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGCTCAATACAAATTAA		
SEQ: 014-391 (badius)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGCTCAATACAAATTAA		
SEQ: 015-391 (badius)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGCTCAATACAAATTAA		
SEQ: 016-391 (badius)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGCTCAATACAAATTAA		
SEQ: 017-391 (badius)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGCTCAATACAAATTAA		
SEQ: 018-391 (badius)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGCTCAATACAAATTAA		
SEQ: 019-391 (badius)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGCTCAATACAAATTAA		
SEQ: 020-391 (badius)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGGCTCAATACAAATTAA		

Figure 3i

[illegible]

Figure 4a





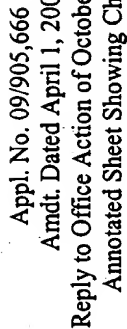
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delete

151 225

SEQ: 021-1f15 (G2)	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 022-3C12	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 023-3N19 (G2)	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 024-2C2	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 025-2C3	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 026-2F11	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 027-KV11 (6C7)	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 028-KV6 (3A1)	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 029-KV2 (2D1)	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 030-N2.5	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 031-KV5 (2H6)	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 032-3E5	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 033-G2.1	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 034-3H24 (G2)	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 035-KV10 (4G6)	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 036-KV12 (6D4)	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 037-N2.2	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 038-N2.3	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 039-N2.1	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 040-KV4 (2E12)	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 041-KV9 (4C6)	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 042-7D6	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 043-3E2	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 044-2D11 (G2)	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 045-3C23 (G2)	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 046-G2.3	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 047-2A3	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 048-2F4	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 049-2B9 (G2)	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 050-2C5	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 051-KV1 (2A6)	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 052-2D13 (G2)	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 053-3C8	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA
SEQ: 054-2D5	(151)	TGGCCCGGTATTATTCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

Figure 4c



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Annotated Sheet Showing Changes

SEQ: 021-1F15 (G2)
 SEQ: 022-3C12
 SEQ: 023-3N19 (G2)
 SEQ: 024-G2.2
 SEQ: 025-2C3
 SEQ: 026-2F11
 SEQ: 027-KV11 (6C7)
 SEQ: 028-KV6 (3A1)
 SEQ: 029-KV2 (2D1)
 SEQ: 030-N2.5
 SEQ: 031-KV5 (2H6)
 SEQ: 032-3E5
 SEQ: 033-G2.1
 SEQ: 034-3H24 (G2)
 SEQ: 035-KV10 (4B6)
 SEQ: 036-KV12 (6D4)
 SEQ: 037-N2.2
 SEQ: 038-N2.3
 SEQ: 039-N2.1
 SEQ: 040-KV4 (2E1.2)
 SEQ: 041-KV9 (4C6)
 SEQ: 042-7D6
 SEQ: 043-3F3
 SEQ: 044-2D11 (G2)
 SEQ: 045-3C23 (G2)
 SEQ: 046-G2.3
 SEQ: 047-2A3
 SEQ: 048-2F4
 SEQ: 049-2B9 (G2)
 SEQ: 050-QC5
 SEQ: 051-KV1 (2A6)
 SEQ: 052-2D13 (G2)
 SEQ: 053-3C8
 SEQ: 054-2D5

Figure 4d



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SEQ: 021-1N15 (G2)	(301)	GC	TTGGCGGCACGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC	301	375
SEQ: 022-3C12	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 023-3N19 (G2)	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 024-G2.2	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 025-2C3	(301)	CA	TTGGTAGAGCAAAACGGACTCGTTCAAGCAGAGATTTACAGGCACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 026-2F11	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 027-FR1X (6C7)	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 028-KV6 (3A1)	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 029-KV2 (2D1)	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 030-N2.5	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 031-KV5 (2H6)	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 032-3E5	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 033-N2.1	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 034-3H24 (G2)	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 035-KV10 (4G6)	(301)	AC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 036-KV12 (6D4)	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 037-N2.2	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 038-N2.3	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 039-N2.1	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 040-KV4 (2E12)	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 041-KV9 (4C6)	(301)	AC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 042-7D6	(301)	AC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 043-3F3	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 044-2D11 (G2)	(301)	AC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 045-3C23 (G2)	(301)	AC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 046-G2.3	(301)	AC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 047-2A3	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 048-2F4	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 049-2B9 (G2)	(301)	AC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 050-2C5	(301)	AC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 051-KV1 (2A6)	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 052-2D13 (G2)	(301)	GC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 053-3C8	(301)	AC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 054-2D5	(301)	AC	TTGGCGGCAGAACCGGTCGACGACAAAGCGGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		

Figure 4e

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Deleuze

Figure 4f



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Annotated Sheet Showing Changes

525

451

SEQ: 021-1f15 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 022-3C22 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 023-3N19 (G2) (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 024-G2.2 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 025-2C3 (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 026-2F11 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 027-KV11 (6Z7) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 028-KV6 (2A1) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 029-KV2 (2D1) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 030-N2.5 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 031-KV5 (2H6) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 032-3E5 (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 033-G2.1 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 034-3H24 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 035-KV10 (4G6) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 036-KV12 (6P4) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 037-N2.2 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 038-N2.3 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 039-N2.1 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 040-KV4 (2E2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 041-KV9 (4C6) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 042-7D6 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 043-3F3 (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 044-2D11 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 045-3C23 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 046-G2.3 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 047-2A3 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 048-2F4 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 049-2B9 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 050-2G5 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 051-KV1 (2A6) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 052-2D13 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 053-3C8 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 054-2D5 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

Figure 49



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delete

	526	544
SEQ: 021-1f15 (G2)	(526)	GGGACTCAATACGAATTGA
SEQ: 022-3012	(526)	GGGACTCAATACGAATTGA
SEQ: 023-3N19 (G2)	(526)	GGGACTGAATACAAAATTGA
SEQ: 024-G2.2	(526)	GGGACTCAATACGAATTGA
SEQ: 025-2C3	(526)	GGGCCACAATACGAATTGA
SEQ: 026-2F11	(526)	AGGCTTAAATACGAATTGA
SEQ: 027-KV11 (6C7)	(526)	GGGCTTAAATACAAAATTGA
SEQ: 028-KV6 (3A1)	(526)	GGGCTTAAATACAAAATTGA
SEQ: 029-KV2 (2D1)	(526)	GGGCCAAAATACAAAATTGA
SEQ: 030-N2.5	(526)	GGGCCACAATACAAAATTGA
SEQ: 031-KV5 (2H6)	(526)	GGGCTTGAATACAAAATTGA
SEQ: 032-3E5	(526)	GGGCTTCAATACGAATTGA
SEQ: 033-G2.1	(526)	GGGACTCAATACGAATTGA
SEQ: 034-3H24 (G2)	(526)	GGGACTCAATACGAATTGA
SEQ: 035-KV10 (4G6)	(526)	GGGCCACAATACAAAATTGA
SEQ: 036-KV12 (6D4)	(526)	AGGCCACAATACAAAATTGA
SEQ: 037-N2.2	(526)	AGGCCACAATACAAAATTGA
SEQ: 038-N2.3	(526)	AGGCCACAATACAAAATTGA
SEQ: 039-N2.1	(526)	AGGCCACAATACAAAATTGA
SEQ: 040-KV4 (2E12)	(526)	GGGCCACAATACAAAATTGA
SEQ: 041-KV9 (4C6)	(526)	GGGCCACAATACGAATTGA
SEQ: 042-7D6	(526)	GGGATTAAATACGAATTGA
SEQ: 043-3F3	(526)	GGGCCAGAATACGAATTGA
SEQ: 044-2D11 (G2)	(526)	AGGCCAGAATACGAATTGA
SEQ: 045-3C23 (G2)	(526)	GGGCCACAATACGAATTGA
SEQ: 046-G2.3	(526)	GGGCCAGAATACGAATTGA
SEQ: 047-2A3	(526)	AGGCTTAAATACAAAATTGA
SEQ: 048-2F4	(526)	AGGCCAGAATACGAATTGA
SEQ: 049-2B9 (G2)	(526)	AGGCCAAAATACGAATTGA
SEQ: 050-2C5	(526)	AGGCCAAAATACGAATTGA
SEQ: 051-KV1 (2A6)	(526)	GGGCCAGAATACGAATTGA
SEQ: 052-2D13 (G2)	(526)	AGGCCAAAATACGAATTGA
SEQ: 053-3C8	(526)	GGGCCAAAATACAAAATTGA
SEQ: 054-2D5	(526)	AGGACAAAATACAAAATTGA

Figure 4h



SEQ: 0551-405 (pumilus)	(1)	--MKFVKRRRIIALVTILVLSVTSLFAMQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	40
SEQ: 0561-406 (subtilis)	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 0571-402 (negat.)	(1)	--MKFVKRRRIIALVTILVLSVTSLFAMQP-SAKAA	-1	DTIQLLWFTGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 0581-400 (lentus)	(1)	--MKFVKRRRIIALVTILVLSVTSLFAMQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 0591-396 (circul.)	(1)	--MKFVKRRRIIALVTILVLSVTSLFAMQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 0601-392 (azotox.)	(1)	--MKFVKRRRIIALVTILVLSVTSLFAMQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 0611-398 (firmus)	(1)	--MKFVKRRRIIALVTILVLSVTSLFAMQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 0621-393 (badius)	(1)	--MKFVKRRRIIALVTILVLSVTSLFAMQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 0631-Dc5h	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 0641-Dc5f	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 0651-Dc5c1	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 0661-Dc5a2	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 0671-Dc512	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 0681-Sga	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 0691-Sgc	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 0701-Sgd	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 0711-Sgf	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 0721-Sgh	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 0731-Mt2b1	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 0741-H2a	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA	-1	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	

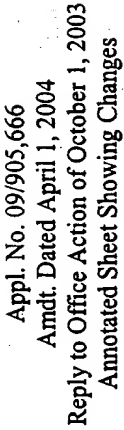
Figure 5a



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116
SEQ:0551-405 (pumilus) (148) TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNAQIHGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
SEQ:0561-406 (subtilis) (148) TDPNQKILYTSIYSSADMIVN- YLSRLDGARNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGLNTN
SEQ:057-402 (negat.) (148) TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ:058-400 (lentus) (148) TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGGLNTN
SEQ:059-396 (circul.) (148) TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGGLDTN
SEQ:060-392 (azotoi.) (148) TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGGLDTN
SEQ:061-398 (firmus) (148) TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNAQIHGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ:062-393 (badius) (148) TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ:063-395 (Dc5h) (148) TDPNQKILYTSIYSSADMIVMN- YLSRLDGARNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGGLNTN
SEQ:064-395f (148) TDPNQKILYTSVYSSADLIIVN- SLSRLIGARNILIHGVGHIGLLTSSQVKGVIKEGLNGGGGLNTN
SEQ:065-395c1 (151) TDPNQKILYTSVYSSADLIIVN- SLSRLIGARNVLIHGUVGHIGLLTSSQVKGVIKEGLNGGGQNTN
SEQ:066-395a2 (151) TDPNQKILYTSVYSSADLIIVN- SLSRLIGARNVLIHGUVGHIGLLTSSQVKGVIKEGLNGGGQNTN
SEQ:067-39512 (151) TDPNQKILYTSVYSSADLIIVN- SLSQFNWRKKHPDPGVGHIGLLTSSQVKGVIKEGLNGGGGLNTN
SEQ:068-395a (148) TDPNQKILYTSVYSSADMIVMN- YLSKLDGAKNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGGLNTN
SEQ:069-395c (148) TDPNQKILYTSVYSSADMIVMN- YLSKLDGAKNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGGLNTN
SEQ:070-395d (148) TDPNQKILYTSVYSSADMIVMN- YLSKLDGAKNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGGLNTN
SEQ:071-395f (148) TDPNQKILYTSVYSSADLIIVN- SLSRLIGARNVQIHGVGHIGLLTSSQVKGVIKEGLNGGGGLNTN
SEQ:072-395h (148) TDPNQKILYTSVYSSADLIIVN- SLSRLIGARNVQIHGVGHIGLLTSSQVKGVIKEGLNGGGQNTN
SEQ:073-Mt2b1 (151) TDPNQKILYTSVYSSADLIIVN- SLSRLTGARNVLIHGUVGHIGLLTSSQVKGVIKEGLNGGGGLNTN
SEQ:074-H2a (148) TDPNQKILYTSVYKLSRSHCRQQLSFNLQETVQIHGVGHIGLLTSSQVKGVIKEGLNGGGGLNTN

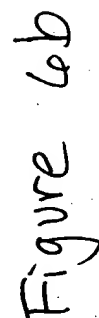
Figure 5c

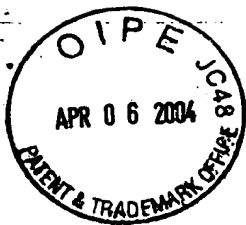


1

SEQ: 075-1f15 (G2)
 SEQ: 076-3012
 SEQ: 077-3N19 (G2)
 SEQ: 078-G2.2
 SEQ: 079-2C3
 SEQ: 080-2F11
 SEQ: 081-KV11 (6C7)
 SEQ: 082-KV6 (3A1)
 SEQ: 083-KV2 (2D4)
 SEQ: 084-N2.1
 SEQ: 085-KV5 (2H6)
 SEQ: 086-3E5
 SEQ: 087-G2.1
 SEQ: 088-3H24 (G2)
 SEQ: 089-KV10 (4G6)
 SEQ: 090-KV12 (6D4)
 SEQ: 091-N2.2
 SEQ: 092-N2.3
 SEQ: 093-N2.1
 SEQ: 094-KV4 (2E12)
 SEQ: 095-KV9 (4C6)
 SEQ: 096-7D6
 SEQ: 097-3F3
 SEQ: 098-2D11 (G2)
 SEQ: 099-3C23 (G2)
 SEQ: 100-G2.3
 SEQ: 101-2A3
 SEQ: 102-2F4
 SEQ: 103-2B9 (G2)
 SEQ: 104-2C5
 SEQ: 105-KV1 (2A6)
 SEQ: 106-2D13 (G2)
 SEQ: 107-3C8
 SEQ: 108-2D5

Figure 6a





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Delete

	151	180
SEQ: 075-1F15 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 076-3C12	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 077-3N19 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 078-G2.2	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 079-2C3	(151)	HGVGHIGLLTSSQVKGVIKEGLNGGGLNTN
SEQ: 080-2F11	(151)	HGVGHIGLLMNSQVKGVIKEGLNGGGLNTN
SEQ: 081-KV11 (6C7)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 082-KV8 (3A1)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 083-KV2 (2D1)	(151)	HGVGHIGLLYSSQVNSLIKEGLNGGGLNTN
SEQ: 084-N2.5	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 085-KV5 (2H6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 086-3E5	(151)	HGVGHIGLLYSSQVNSLIKEGLNGGGLNTN
SEQ: 087-G2.1	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 088-3H24 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 089-KV10 (4G6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 090-KV12 (6D4)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 091-N2.2	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 092-N2.3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 093-N2.1	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 094-KV4 (2E12)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 095-KV9 (4C6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 096-YD6	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 097-3F3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 098-2D11 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 099-3C23 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 100-G2.3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 101-2A1	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 102-2F4	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 103-2B9 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 104-2E5	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 105-KV11 (2A6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 106-2D13 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 107-3E8	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 108-2D5	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN

Figure 6c



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1 75

SEQ: 001	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCAGTCACATCGC
SEQ: 002	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC
SEQ: 003	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCAGTCACATCGC
SEQ: 004	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCAGTCACATCGC
SEQ: 005	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCAGTCACATCGC
SEQ: 006	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCAGTCACATCGC
SEQ: 007	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCAGTCACATCGC
SEQ: 008	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCAGTCACATCGC
SEQ: 009	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCAGTCACATCGC
SEQ: 010	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC
SEQ: 011	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC
SEQ: 012	(1)	ATGAAAGTGATTTTGTAAAGAAAAGGAGT-TTGCAAAATTCCTTGGTCCCTTAGTGCTAGGTTCAATAGC
SEQ: 013	(1)	ATGAAAGTGATTTTGTAAAGAAAAGGAGT-TTGCAAAATTCCTTGGTCCCTTAGTGCTAGGTTCAATAGC
SEQ: 014	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC
SEQ: 015	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC
SEQ: 016	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC
SEQ: 017	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC
SEQ: 018	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC
SEQ: 019	(1)	ATGAAAGTGATTTTGTAAAGAAAAGGAGT-TTGCAAAATTCCTTGGTCCCTTAGTGCTAGGTTCAATAGC
SEQ: 020	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC

FIGURE 3a



		(Signal peptide coding region)	(Mature coding region)
SEQ: 001	76	TGTTTGGGATGCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 002	(65)	TGTTTGGGATGCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 003	(65)	TGTTTGGGATGCAGCCGTCAGCAAAAGCCGCT	GA-CACAATCCAGTTGTTATGTTTCACACTGTTTCACGGAGGAGCT
SEQ: 004	(65)	TGTTTGGGATGCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 005	(65)	TGTTTGGGATGCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 006	(65)	TGTTTGGGATGCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 007	(65)	TGTTTGGGATGCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 008	(65)	TGTTTGGGATGCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 009	(65)	TGTTTGGGATGCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 010	(65)	TGTTTGGGATGCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 011	(75)	CTTCATCCAGCCGAAAGAGCCAAA-GCGGCT	GAGCATAATCCGGTTGTAATGTTGCAT-GGCATGGGTGGTGCG
SEQ: 012	(75)	CTTCATCCAGCCGAAAGAGATCAGA-GCGGCT	GAGCATAATCCGGTTGTTATGTTGCAT-GGCATGGGTGGTGCG
SEQ: 013	(75)	GTTTATCCAGCCGAAAGAGGCGAAG-GCGGCT	GAGCATAATCCGGTTGTTATGTTGCAT-GGCATGGGTGGTGCG
SEQ: 014	(65)	TGTTTGGGATGCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 015	(65)	TGTTTGGGATGCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 016	(65)	TGTTTGGGATGCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 017	(65)	TGTTTGGGATGCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 018	(65)	TGTTTGGGATGCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 019	(75)	CTTCATCCAGCCGAAAGAAATCAAA-GCAGCT	GAGCACAATCCGGTTGTTATGTTGCAT-GGTATCGGAGGAGCT
SEQ: 020	(65)	TGTTTGGGATGCAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT

FIGURE 3b



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151

SEQ: 001	(139)	TCATACAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAACGGGCAAGCTGTATGCGGTTGAT
SEQ: 002	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAACGGGCAAGCTGTATGCGGTTGAT
SEQ: 003	(139)	TCATACAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAACGGGCAAGCTGTATGCGGTTGAT
SEQ: 004	(139)	TCATACAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAACGGGCAAGCTGTATGCGGTTGAT
SEQ: 005	(139)	TCATACAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAACGGGCAAGCTGTATGCGGTTGAT
SEQ: 006	(139)	TCATACAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAACGGGCAAGCTGTATGCGGTTGAT
SEQ: 007	(139)	TCATACAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAACGGGCAAGCTGTATGCGGTTGAT
SEQ: 008	(139)	TCATACAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAACGGGCAAGCTGTATGCGGTTGAT
SEQ: 009	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAACGGGCAAGCTGTATGCGGTTGAT
SEQ: 010	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAACGGGCAAGCTGTATGCGGTTGAT
SEQ: 011	(148)	TCTTATAACTTTTGGCTTCGATCAAAACGATACTTAGTATCACAGGGATGGGATCAAAACCACTTTTGGCAATCGAT
SEQ: 012	(148)	TCTTATAACTTTTGGCTTCGATCAAAACGATACTTAGTATCACAGGGATGGGATCAAAACCACTTTTGGCAATCGAT
SEQ: 013	(148)	TCTTATAACTTTTGGCTTCGATCAAAACGATACTTAGTATCACAGGGATGGGATCAAAACCACTTTTGGCAATCGAT
SEQ: 014	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAACGGGCAAGCTGTATGCGGTTGAT
SEQ: 015	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAACGGGCAAGCTGTATGCGGTTGAT
SEQ: 016	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAACGGGCAAGCTGTATGCGGTTGAT
SEQ: 017	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAACGGGCAAGCTGTATGCGGTTGAT
SEQ: 018	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAACGGGCAAGCTGTATGCGGTTGAT
SEQ: 019	(148)	TCTTATAACTTTTGGCTTCGATCAAAACGATACTTAGTATCACAGGGATGGGATCAAAACCACTTTTGGCAATCGAT
SEQ: 020	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAACGGGCAAGCTGTATGCGGTTGAT

FIGURE 3c



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226
SEQ: 001 (214) TTTTGGGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAA
SEQ: 002 (214) TTTTGGGACAAGACAGGACGAATTATAACAATGGACCGGTATTACCACGATTGTGCAAAAGGTTTAGATGAA
SEQ: 003 (214) TTTTGGGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAA
SEQ: 004 (214) TTTTGGGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAA
SEQ: 005 (214) TTTTGGGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAA
SEQ: 006 (214) TTTTGGGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAA
SEQ: 007 (214) TTTTGGGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAA
SEQ: 008 (214) TTTTGGGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAA
SEQ: 009 (214) TTCAAGGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGATGAA
SEQ: 010 (214) TTCTAAGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGACAAA
SEQ: 011 (223) TTCATAGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGACAAA
SEQ: 012 (223) TTCATAGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGACAAA
SEQ: 013 (223) TTCATAGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGACAAA
SEQ: 014 (214) TTCAGGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGATGAA
SEQ: 015 (214) TTCTGGGATAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGATGAA
SEQ: 016 (214) TTCTGGGATAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGATGAA
SEQ: 017 (214) TTCAAGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGACAAA
SEQ: 018 (214) TTCATTGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGACAAA
SEQ: 019 (223) TTCATAGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGACAAA
SEQ: 020 (214) TTCAGGACAAGACAGGACGAATTATAACAATGGCCGGTATTATCACGATTGTGCAAAAGGTTTAGACAAA

FIGURE 3d



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301

SEQ: 001	(289)	ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGTATGGGTGGCGGGAACACACCTTACTACATAAAAAATCTG
SEQ: 002	(289)	ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGGGCGGGAACACACTTTACTACATAAAAAATCTG
SEQ: 003	(289)	ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTG
SEQ: 004	(289)	ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTG
SEQ: 005	(289)	ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTG
SEQ: 006	(289)	ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTG
SEQ: 007	(289)	ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTG
SEQ: 008	(289)	ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTG
SEQ: 009	(289)	ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTG
SEQ: 010	(289)	ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTG
SEQ: 011	(298)	ACGGGTGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGGTGGAGCGGAACACGCTATACTATATCAAGAAATCTA
SEQ: 012	(298)	ACGGGTGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGGTGGAGCGGAACACGCTATACTATATTAAGAAATCTA
SEQ: 013	(298)	ACGGGTGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGGTGGAGCGGAACACGCTATACTATATCAAGAAATCTA
SEQ: 014	(289)	ACCGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGGGCGGCTAACACGCTTTACTACATAAAAAATTTG
SEQ: 015	(289)	ACCGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGGGCGGCTAACACGCTTTACTACATAAAAAATTTG
SEQ: 016	(289)	ACCGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGGGCGGCTAACACGCTTTACTACATAAAAAATTTG
SEQ: 017	(289)	ACAGGAGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGGGGAGCGGAACACATTATATACTATATTAAGAAATCTA
SEQ: 018	(289)	ACAGGAGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGGGGAGCGGAACACATTATATACTATATTAAGAAATCTA
SEQ: 019	(298)	ACGGGTGCCAAAAAAGTAGATATTGTGGCGCATAGTATGGGGGCGGGAACACGCTATACTATATTAAGAAATCTA
SEQ: 020	(289)	ACGGGTGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGGGGCGGGAACACGCTATACTATATTAAGAAATCTA

FIGURE 3e

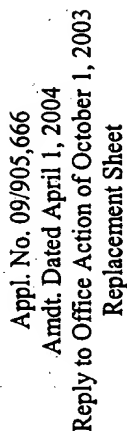


FIGURE 3f

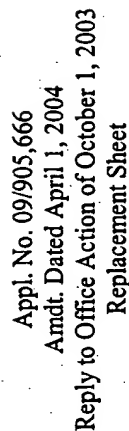
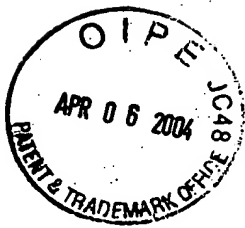


FIGURE 3g



Appl. No. 09/905,666
Amdt. Dated April 1, 2004
Reply to Office Action of October 1, 2003
Replacement Sheet

526

600

SEQ: 001
SEQ: 002
SEQ: 003
SEQ: 004
SEQ: 005
SEQ: 006
SEQ: 007
SEQ: 008
SEQ: 009
SEQ: 010
SEQ: 011
SEQ: 012
SEQ: 013
SEQ: 014
SEQ: 015
SEQ: 016
SEQ: 017
SEQ: 018
SEQ: 019
SEQ: 020

(513) ATCAAAATTAGACGGT-GCTAAAAAC-GCTCAAAATTCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAA
(513) ATCAAGATTAGATGGT-GCTAGAAAC-GTTCAAAATCCATGGCGTTGGACACATCGGCCCTTCTGTACAGCAGCCAA
(513) ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAA
(513) ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAA
(513) ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAA
(513) ATCAAAATTAGACGGT-GCTAAAAAC-GTACAAATTCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAA
(513) ATCAAAATTAGACGGT-GCTAAAAAC-GCTCAAAATTCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAA
(513) ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAA
(513) ATCAAGATTAGATGGT-GCGAGAAAC-GTTCAAAATCCATGGCGTTGGACACATCGGCCCTTCTGTACAGCAGCCAA
(513) CTCCTCGTTTAATTGGC-GCAAGAAAC-ATCCTGATCCATGGCGTTGGTCATATCGGTCCTATTAACTCAAGCCAA
(522) TTCGC-GTTTAAATTGGCGCAAGAAAC-GTCTGATCCACGGCGTTGGACATATCGGTCCTATTAACTCAAGCCAA
(522) CTCGC-GTTTAAATTGGCGCAAGAAAC-GTCTCATTCACGGCGTTGGTCACATCGGTCCTATTAGCTTCAAGCCAA
(522) CTCCTAGTTTAAATTGGCGCAAGAAAC-ATCCTGATCCA-GGCGTTGGTCATATCGGTCCTATTAACTCAAGCCAA
(513) AACAAAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTCTGGACATATCGGCCCTTCTGTACAGCAGCCAA
(513) ATCAAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTCTGGACATATCGGCCCTTCTGTACAGCAGCCAA
(513) ATCAAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTCTGGACATATCGGCCCTTCTGTACAGCAGCCAA
(513) ATCAAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTCTGGACATATCGGCCCTTCTGTACAGCAGCCAA
(513) CTCCTCGTTTAAATTGGC-GCAAGAAAC-GTCCAAATCCATGGCGTTGGACATATCGGTCCTATTAACTCAAGCCAA
(513) CTCCTCGTTTAAATTGGC-GCAAGAAAC-GTCCAAATCCATGGCGTTGGACATATCGGTCCTATTAACTCAAGCCAA
(522) TTCGC-GTTTAACTGGCGCAAGAAAT-GTCTGATCCACGGCGTTGGCCATATCGGTCCTATTAACTCAAGCCAA
(514) CTCCTCGTTTAAATTGGCTGCAAGAAACAGTCCAAATCCATGGCGTTGGACATATCGGTCCTATTAACTCAAGCCAA

FIGURE 3h



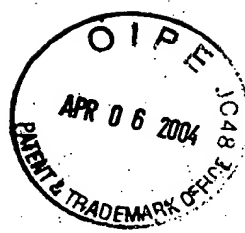
Appl. No. 09/905,666
Amdt. Dated April 1, 2004
Reply to Office Action of October 1, 2003
Replacement Sheet

601 654

SEQ: 001 (586) GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCCAAAATACGAATTAA
SEQ: 002 (586) GTCAACAGCCTGATTAAAGAGGCTGAACGGCGGGGACTCAATACAAATTAG
SEQ: 003 (586) GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCCACAATACAAATTAA
SEQ: 004 (586) GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGACTAAATACAAATTAA
SEQ: 005 (586) GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCTCAATACAAATTAA
SEQ: 006 (586) GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCTAGATACAAATTAA
SEQ: 007 (586) GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGAGGCCACAATACAAATTAA
SEQ: 008 (586) GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGAGGCCACAATACAAATTAA
SEQ: 009 (586) GTCAACAGCCTGATTAAAGAGGCTGAACGGCGGGGGCTCAATACAAATTAA
SEQ: 010 (586) GTGAAAGGGTATATTAAAGAGGACTGAACGGCGGGAGGCTCAATACAAATTAA
SEQ: 011 (595) GTCAAAGGCTATGTGAAAGAGGATTGAATGGCGGGGACAGAAATACAAATTAA
SEQ: 012 (595) GTCAAAGGCTATATCAAAGAGGACTGAATGGCGGGAGGCCAAAATACAAATTAA
SEQ: 013 (595) GTGAAAGGGTATATTAAAGAGGACTGAACGGCGGGAGGCTCAATACAAATTAA
SEQ: 014 (586) GTCAACAGCCTGATTAAAGAGGCTTAACGGCGGGAGGCCCTCAATACAAATTAA
SEQ: 015 (586) GTCAATAGCCTGATTAAAGAGGCTTAACGGCGGGAGGACTCAATACGAATTAA
SEQ: 016 (586) GTCAACAGCCTGATTAAAGAGGCTTAACGGCGGGGGCTGAATACGAATTAA
SEQ: 017 (586) GTCAAAGGATATATTAAAGAGGACTGAACGGCGGGGGCTCAATACAAATTAA
SEQ: 018 (586) GTCAAAGGATATATTAAAGAGGACTGAACGGCGGGAGGCCAAAATACAAATTAA
SEQ: 019 (595) GTGAAAGGGTATATTAAAGAGGACTGAACGGCGGGGGCTAAATACAAATTAA
SEQ: 020 (589) GTCAAAGGATATATTAAAGAGGACTGAACGGCGGGGACTAAATACAAATTAA

FIGURE 3i

FIGURE 4a



150

76

SEQ: 021 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 022 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 023 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 024 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 025 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 026 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 027 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 028 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 029 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 030 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 031 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 032 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 033 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 034 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 035 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 036 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 037 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 038 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 039 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 040 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 041 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 042 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 043 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 044 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 045 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 046 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 047 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 048 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 049 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 050 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 051 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 052 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 053 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

SEQ: 054 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA

FIGURE4b



225

151

SEQ: 021 (151) TGGCCCGGTATTATCGCGGTATTGCGAAAGGTTATTAGATGAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 022 (151) TGGCCCGGTATTATCTAGATCGTCAAGATGTGCTAGACAAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 023 (151) TGGCCCGGTATTATCAGCATTTGTGAAAGGTTATTAGATGAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 024 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 025 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 026 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 027 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 028 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 029 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 030 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 031 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 032 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 033 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 034 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 035 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 036 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 037 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 038 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 039 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 040 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 041 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 042 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 043 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 044 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 045 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 046 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 047 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 048 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 049 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 050 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 051 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 052 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 053 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA
SEQ: 054 (151) TGGCCCGGTATTATCAGCATTTGTGCAAGGTTTTAGACGAAACCGGTGCGGAAAGGTTGGATATTTGTCGCTCA

FIGURE 4c

FIGURE 4d



375

FIGURE 4e



376 450

SEQ: 021 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAATGTTCAAAT

SEQ: 022 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGGCTAAAAATGTTCAAAT

SEQ: 023 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 024 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 025 (376) ATCCGTCATAGCTCAGCAGATCTTATTGTCGTCACAGTCTCTCTGTTTAAATGTCGCAAGAAACGTTCAAAT

SEQ: 026 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 027 (376) ATCCGTTTACAGTAGTGTCTGATATGATTGTTTATGAATTAATCTATCAAAATTAAGACGGGCTAAAAATGTTCAAAT

SEQ: 028 (376) ATCCGTTTACAGTAGTGTCTGATATGATTGTTTATGAATTAATCTATCAAAATTAAGACGGGCTAAAAATGTTCAAAT

SEQ: 029 (376) ATCCGTTTACAGTAGTGTCTGATATGATTGTTTATGAATTAATCTATCAAAATTAAGACGGGCTAAAAATGTTCAAAT

SEQ: 030 (376) ATCCGTTTACAGTAGTGTCTGATATGATTGTTTATGAATTAATCTATCAAAATTAAGACGGGCTAAAAATGTTCAAAT

SEQ: 031 (376) ATCCGTTTACAGTAGTGTCTGATATGATTGTTTATGAATTAATCTATCAAAATTAAGACGGGCTAAAAATGTTCAAAT

SEQ: 032 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGGCTAAAAATGTTCAAAT

SEQ: 033 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGGCTAAAAATGTTCAAAT

SEQ: 034 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGGCTAAAAATGTTCAAAT

SEQ: 035 (376) ATCCATTACAGCAGTCCGATATGAATGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 036 (376) ATCCGTTTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 037 (376) ATCCGTTTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 038 (376) ATCCGTTTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 039 (376) ATCCGTTTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 040 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 041 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGGCTAAAAATGTTCAAAT

SEQ: 042 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 043 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 044 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 045 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 046 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 047 (376) ATCCGTTTACAGTAGTGTCTGATATGATTGTTTATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 048 (376) ATCCGTTTACAGTAGTGTCTGATATGATTGTTTATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 049 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGGCTAAAAATGTTCAAAT

SEQ: 050 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 051 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 052 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 053 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAACGTTCAAAT

SEQ: 054 (376) ATCCATTACAGCAGTCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGTAAAAATGTTCAAAT

FIGURE 4f

[illegible]

FIGURE 4g



SEQ: 021	526	(526)	GGGACTCAATACGAATTGA
SEQ: 022		(526)	GGGACTCAATACGAATTGA
SEQ: 023		(526)	GGGACTGAATACAAAATTGA
SEQ: 024		(526)	GGGACTCAATACGAATTGA
SEQ: 025		(526)	GGGCCACAATACGAATTGA
SEQ: 026		(526)	AGGCTTAAATACGAATTGA
SEQ: 027		(526)	GGGCTTAAATACAAAATTGA
SEQ: 028		(526)	GGGCTTAAATACAAAATTGA
SEQ: 029		(526)	GGGCCAAAAATACAAAATTGA
SEQ: 030		(526)	GGGCCACAATACAAAATTGA
SEQ: 031		(526)	GGGCTTGAATACAAAATTGA
SEQ: 032		(526)	GGGCTTCAATACGAATTGA
SEQ: 033		(526)	GGGACTCAATACGAATTGA
SEQ: 034		(526)	GGGACTCAATACGAATTGA
SEQ: 035		(526)	GGGCCACAATACAAAATTGA
SEQ: 036		(526)	AGGCCACAATACAAAATTGA
SEQ: 037		(526)	AGGCCACAATACAAAATTGA
SEQ: 038		(526)	AGGCCACAATACAAAATTGA
SEQ: 039		(526)	AGGCCACAATACAAAATTGA
SEQ: 040		(526)	GGGCCACAATACAAAATTGA
SEQ: 041		(526)	GGGCCACAATACGAATTGA
SEQ: 042		(526)	GGGATTAAATACGAATTGA
SEQ: 043		(526)	GGGCCAGAATACGAATTGA
SEQ: 044		(526)	AGGCCAGAATACGAATTGA
SEQ: 045		(526)	GGGCCACAATACGAATTGA
SEQ: 046		(526)	GGGCCAGAATACGAATTGA
SEQ: 047		(526)	AGGCTTAAATACAAAATTGA
SEQ: 048		(526)	AGGCCAGAATACGAATTGA
SEQ: 049		(526)	AGGCCAAAAATACGAATTGA
SEQ: 050		(526)	AGGCCAAAAATACGAATTGA
SEQ: 051		(526)	GGGCCAGAATACGAATTGA
SEQ: 052		(526)	AGGCCAAAAATACGAATTGA
SEQ: 053		(526)	GGGCCAAAAATACAAAATTGA
SEQ: 054		(526)	AGGACAAAAATACAAAATTGA

FIGURE 4h



		(Signal peptide)	(Mature region)	
SEQ: 055	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	40
SEQ: 056	(1)	--MKFVKRRRIIALVTILVLSVTSLSFALQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 057	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	DTIQLLWFTGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 058	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 059	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 060	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 061	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 062	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 063	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 064	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 065	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 066	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 067	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 068	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 069	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 070	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 071	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 072	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 073	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 074	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPMVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	

FIGURE 5a



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SEQ: 055 (73) WDKTGTNNNGPVLRSFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPG

SEQ: 056 (73) WDKTGTNNNGPVLRSFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTGKALPG

SEQ: 057 (73) WDKTGTNNNGPVLRSFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTGKALPG

SEQ: 058 (73) WDKTGTNNNGPVLRSFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTGKALPG

SEQ: 059 (73) WDKTGTNNNGPVLRSFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTGKALPG

SEQ: 060 (73) WDKTGTNNNGPVLRSFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTGKALPG

SEQ: 061 (73) WDKTGTNNNGPVLRSFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTGKALPG

SEQ: 062 (73) WDKTGTNNNGPVLRSFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTGKALPG

SEQ: 063 (73) KDKTGTNNNGPVLRSFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTGKALPG

SEQ: 064 (73) XDKTGTNNNGPVLRSFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTGKALPG

SEQ: 065 (76) IDKTGNNLNGPVLRSFVKDVLAKTGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTLGGANGLVSSRALPG

SEQ: 066 (76) IDKTGNNRNGPVLRSFVKDVLAKTGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTLGGANGLVSLRALPG

SEQ: 067 (76) IDKTGNNRNGPVLRSFVKDVLAKTGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTLGGANGLVSLRALPG

SEQ: 068 (73) RDKTGNLNGPVLRSFVKKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTLGGANGLVSSRALPG

SEQ: 069 (73) WDKTGNLNGPVLRSFVKKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLVTGKALPG

SEQ: 070 (73) SDKTGNLNGPVLRSFVKKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLVTGKALPG

SEQ: 071 (73) KDKTGNRNGPVLRSFVKDVLAKTGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTLGGANGLVSSRALPG

SEQ: 072 (73) IDKTGNRNGPVLRSFVKDVLAKTGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTLGGANGLVSSRALPG

SEQ: 073 (76) IDKTGNRNGPVLRSFVKDVLAKTGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTLGGANGLVSLRALPG

SEQ: 074 (73) RDKTGNRNGPVLRSFVKDVLAKTGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTLGGANGLVSSRALPG

FIGURE 5b



SEQ: 055	116	181
SEQ: 056	TDPNQILYTSYSSADMIVMN- YLSKLDGAKNAQIHGVGHI GLLMNSQVNSLIKEGLNGGGQNTN	
SEQ: 057	TDPNQILYTSYSSADMIVN- YLSRLDGARNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGLNTN	
SEQ: 058	TDPNQILYTSYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGHNTN	
SEQ: 059	TDPNQILYTSYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 060	TDPNQILYTSYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGGLNTN	
SEQ: 061	TDPNQILYTSYSSADMIVMN- YLSKLDGAKNAQIHGVGHI GLLMNSQVNSLIKEGLNGGGHNTN	
SEQ: 062	TDPNQILYTSYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGHNTN	
SEQ: 063	TDPNQILYTSYSSADMIVMN- YLSRLDGARNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGLNTN	
SEQ: 064	TDPNQILYTSYSSADLIWN- SLSRLIGARNVLIHGVLIGLLTSSQVKGVIKEGLNGGGGLNTN	
SEQ: 065	TDPNQILYTSYSSADLIWN- SLSRLIGARNVLIHGVLIGLLTSSQVKGVIKEGLNGGGQNTN	
SEQ: 066	TDPNQILYTSYSSADLIWN- SLSRLIGARNVLIHGVLIGLLTSSQVKGVIKEGLNGGGQNTN	
SEQ: 067	TDPNQILYTSYSSADLIWN- SLSQFNWRKKHPDPGVGHI GLLTSSQVKGVIKEGLNGGGLNTN	
SEQ: 068	TDPNQILYTSYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGLNTN	
SEQ: 069	TDPNQILYTSYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGLNTN	
SEQ: 070	TDPNQILYTSYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGLNTN	
SEQ: 071	TDPNQILYTSYSSADLIWN- SLSRLIGARNVQIHGVGHI GLLTSSQVKGVIKEGLNGGGLNTN	
SEQ: 072	TDPNQILYTSYSSADLIWN- SLSRLIGARNVQIHGVGHI GLLTSSQVKGVIKEGLNGGGQNTN	
SEQ: 073	TDPNQILYTSYSSADLIWN- SLSRLTGARNVLIHGVLIGLLTSSQVKGVIKEGLNGGGLNTN	
SEQ: 074	TDPNQILYTSVYKLSRSHCRQQLSFNWLQETVQIHGVGHI GLLTSSQVKGVIKEGLNGGGLNTN	

FIGURE 5c



1 75

SEQ: 075 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 076 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 077 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 078 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 079 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 080 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 081 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 082 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 083 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 084 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 085 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 086 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 087 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 088 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 089 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 090 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 091 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 092 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 093 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 094 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 095 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 096 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 097 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 098 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 099 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 100 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 101 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 102 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 103 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 104 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 105 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 106 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 107 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

SEQ: 108 (1) EHNPMVHVHIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNYNNGPVL SRFVKKVLD ETGAKKVD IVAH

FIGURE 6a



150

76

SEQ: 075	(76)	SMGGANTLYYIKNLDGGNKVENVVTGGTNRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 076	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 077	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 078	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 079	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANGLVSSRALPGTDPNQKILYTSIYSSADLIVNLSRLIGARNVQI
SEQ: 080	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSRALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 081	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 082	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 083	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 084	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 085	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLVTGKALPGTDPNQKILYASVYSSADMIVMNYLSKLDGAKNVQI
SEQ: 086	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 087	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGTNRLTTSRALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 088	(76)	SMGGANTLYYIKNLDGGNKVENVVTGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 089	(76)	SMGGANTLYYIKNLDGGNKVESVVTGGANRLVTGKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 090	(76)	SMGGANTLYYIKNLDGGNKVENVVTGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 091	(76)	SMGGANTLYYIKNLDGGNKVENVVTGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 092	(76)	SMGGANTLYYIKNLDGGNKVENVVTGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 093	(76)	SMGGANTLYYIKNLDGGNKVENVVTGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 094	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 095	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 096	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 097	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 098	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 099	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 100	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 101	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 102	(76)	SMGGANTLYYIKNLDGGDKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 103	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 104	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 105	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 106	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 107	(76)	SMGGANTLYYIKNLDGGNKVENVVTGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 108	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI

FIGURE 6b



151
SEQ: 075 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 076 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 077 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 078 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 079 (151) HGVGHIGLLTSSQVKGVIKEGLNGGGLNTN
SEQ: 080 (151) HGVGHIGLLMNSQVKGVIKEGLNGGGLNTN
SEQ: 081 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 082 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 083 (151) HGVGHIGLLYSSQVNSLIKEGLNGGGLNTN
SEQ: 084 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 085 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 086 (151) HGVGHIGLLYSSQVNSLIKEGLNGGGLNTN
SEQ: 087 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 088 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 089 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 090 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 091 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 092 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 093 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 094 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 095 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 096 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 097 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 098 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 099 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 100 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 101 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 102 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 103 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 104 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 105 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 106 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 107 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 108 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN

FIGURE 6c